OM protein - protein search, using sw model

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GenCore version 5.1.3

Run on: December 19, 2002, 14:53:07 ; Search time 38 Seconds
           (without alignments)
           3079.862 Million cell updates/sec

Title: us-08-813-323B-2
Perfect score: 3008
Sequence: 1 MESSKKMDSPGALQTNPPLK..............IKDDTIFIKVIVDTFSDLPDP 568

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : SPTREMBL_21:*
  1: sp_archea:*
  2: sp_bacteria:*
  3: sp_fungi:*
  4: sp_human:*
  5: sp_invertebrate:*
  6: sp_mammal:*
  7: sp_mhc:*
  8: sp_organelle:*
  9: sp_phage:*
 10: sp_plant:*
 11: sp_rodent:*
 12: sp_virus:*
 13: sp_vertebrate:*
 14: sp_unclassified:*
 15: sp_rvirus:*
 16: sp_bacteriap:*
 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	1253.5	41.7	558	11	Q61480	Q61480 mus musculu
2	1253.5	41.7	558	11	P70191	P70191 mus musculu
3	1192.5	39.6	557	4	O00463	O00463 homo sapien
4	832	27.7	508	11	O54896	O54896 mus musculu
5	717	23.8	447	4	Q96NT2	Q96nt2 homo sapien
6	692	23.0	501	13	Q90WT6	Q90wt6 carassius a
7	560.5	18.6	470	4	Q14848	Q14848 homo sapien
8	560.5	18.6	470	4	Q9BU24	Q9bu24 homo sapien
9	553	18.4	522	4	Q9Y4K3	Q9y4k3 homo sapien
10	536	17.8	530	11	P70196	P70196 mus musculu
11	524.5	17.4	470	11	Q61382	Q61382 mus musculu
12	522.5	17.4	462	5	Q9BIW7	Q9biw7 caenorhabdi
13	522.5	17.4	509	5	O62248	O62248 caenorhabdi
14	506	16.8	486	5	Q9XYR0	Q9xyr0 drosophila
15	503	16.7	412	5	Q9UAC5	Q9uac5 drosophila
16	437.5	14.5	352	6	Q95LR1	Q95lr1 macaca fasc
17	286	9.5	296	12	Q8QUJ9	Q8qu19 infectious
18	286	9.5	452	5	Q960H6	Q960h6 drosophila
19	270	9.0	475	5	Q9UAC4	Q9uac4 drosophila
20	270	9.0	475	5	Q9W319	Q9w319 drosophila
21	268	8.9	475	5	Q9XYQ9	Q9xyq9 drosophila
22	263	8.7	395	5	Q9VXG5	Q9vxg5 drosophila
23	214.5	7.1	198	4	Q75615	Q75615 homo sapien
24	211	7.0	239	11	Q9CQ29	Q9cq29 mus musculu
25	209.5	7.0	594	11	Q922B6	Q922b6 mus musculu
26	207.5	6.9	594	4	Q9H073	Q9h073 homo sapien
27	207	6.9	335	6	Q96CC2	Q96cc2 homo sapien
28	204.5	6.8	1063	11	Q90Y55	Q90y55 mus musculu
29	203.5	6.8	1098	4	Q9UPO7	Q9upo7 homo sapien
30	183.5	6.1	891	13	Q91885	Q91885 xenopus lae
31	183.5	6.1	313	5	Q9N586	Q9n586 caenorhabdi
32	173.5	5.8	33	10	Q9C6H3	Q9c6h3 arabidopsis
33	171	5.7	626	4	Q9Y2K3	Q9y2k3 homo sapien
34	167	5.6	808	11	Q922N9	Q922n9 mus musculu
35	160	5.3	610	4	Q9UNL1	Q9unl1 homo sapien
36	158	5.3	808	4	O15083	O15083 homo sapien
37	154	5.1	1120	13	Q91431	Q91431 xenopus lae
38	153.5	5.1	390	11	Q96EL5	Q96el5 homo sapien
39	152.5	5.1	609	5	Q9VSW7	Q9vsw7 drosophila
40	152.5	5.1	713	11	Q92021	Q92021 homo sapien
41	152.5	5.1	846	13	Q9YHD6	Q9yhd6 rana catesb
42	152	5.1	671	4	O75130	O75130 homo sapien
43	151.5	5.0	1938	11	Q8R205	Q8r205 mus musculu
44	151	5.0	1300	13	Q91BD7	Q91bd7 seriola dum
45	150.5	5.0	4		Q13999	Q13999 homo sapien

ALIGNMENTS

RESULT 1

ID   Q61480   PRELIMINARY;   PRT;   558 AA.
AC   Q61480;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF5.
GN   TRAF5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=96278943; PubMed=8663299;
RA   Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA   Yagita H., Okumura K.;
RT   "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT   the lymphotoxin-beta receptor.";
RL   J. Biol. Chem. 271:14661-14664(1996).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; D78141; BAA11218.1; -.
DR   MGD; MGI:107548; Traf5.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; znf_ring.
DR   InterPro; IPR001293; ZnF_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ   SEQUENCE   558 AA;   64154 MW;   D85E4867462255D42 CRC64;

Query Match   41.7%;   Score 1253.5;   DB 11;   Length 558;

```
Best Local Similarity 41.6%; Pred. No. 8.9e-71;
Matches 241; Conservative 114; Mismatches 166; Indels 59; Gaps 10;

Qy   22  HTDRSAGTP-VFVPEQGG------------YKEKFVKTVEDKYKCEKCHLVLCSPKQTECGH  70
             |::  :| :|                  ||:  :| :||| :|   | |  |||| |||
Db    3  HSEEQAAVPCAFIRQNSGGNSISLDFEPDTEYQFVEQLEERYKCAFCHSVLHNPHQTGCGH  62

Qy   71  RFCESCMAALLS-SSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNESRGCAEQLT  129
          |||  | ::|  |:| ||  ||:||||  |:|||||||||:| | |||:   |||| ::
Db   63  RFCQOCIRSLRELNSVPICPVDKEVIKPQEVFKDNCCKREVLNLHVYCKN-APGCNARII  121

Qy  130  LGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIAL  189
          ||  | :| :|  | ||||  |||||| |||||| |:||||||||| ||:|| |||:|:
Db  122  LGRFQDHLQH-CSFQAVPCPNESCREAMLRKDVKEHLSAYCRFREEKCLYCKRDIVVTNL  180

Qy  190  QKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIK  249
          | |: ||  ||:| || |:||| | |||||||||||:| |  |  ||||| | ||||||
Db  181  QDHEENSCPAYPVSCPNRC-VQTIPRARVNEHLTVCPEAEQDCPFKHYGCTVKGKRGNLL  239

Qy  250  AHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEML  309
          : | ::  ||::::|   :|  |:  | |:::|:| |||| |  ||  |||  ||::|::
Db  240  EHERAALQDHMLIVLEKNYQLEQRISDLYQSLEQKESKIQQLAETVKKFEKELKQFIQMF  299

Qy  310  RNN------------ESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADS          349
          ||                :|:| |:|  | :|::|  | |  |   ||
Db  300  GRNGTFLSNVQALTSHTDKSAWLEAQVRHLLQIVNQQPSRL----------------DLRS 344

Qy  350  MKSSVESLQNRVTELESVDKSACQVARNTGLLESQLSRHDQMLSVHDIIRLADMDLRFQVL  409
              :|:|::|| | || | | || ::| :|||||| ||||::|:||:|:|||||||||
Db  345  ------QRLVLEGETSKHDAHINIHKAQLNKNEERFKQL                       397

Qy  410  ETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGT  469
          | :: :| |||| |||  ||:|||  ::||| |||||| |  |:|||| |||||| ||||
Db  398  EGACYSGKLIWKVTDYRVKKREAVEGHTVSVFSQPFYTSRCGYRLCARAYLNGDGSGKGT  457

Qy  470  HLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSSFKKPTGEMN  529
          ||||:||::|||:|:|| ||||:|||||||||  :: ||  ||| || |||||||:| |||
Db  458  HLSLYFVVWRGEFDSLLQOWPFRQRVTLMLLDQSGKKNHIVETFKADPNSSSSFKRPDGEMN  517

Qy  530  IASGCPVFVAQTVLEN--GTYIKDDTIFIKVIVDTSDLPD                      567
          |||||| ||: ||||   |||||||:|:||:|||:|| |
Db  518  IASGCPRFVSHSTLENSKNTYIKDDTLFLKVAVDLTDLED                      557
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RESULT 2
ID   P70191
AC   P70191;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF5 (Similar to TNF receptor-associated factor 5).
OS   Mus musculus (Mouse).
GN   TRAF5.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96382484; PubMed=8790348;
RA   Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,
RA   Yamamoto T., Inoue J.;
RT   "TRAF5, a novel tumor necrosis factor receptor-associated factor
RT   family protein, mediates CD40 signaling.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; D83528; BAA11942.1; -.
DR   EMBL; BC012702; AAH12702.1; -.
DR   MGD; MGI:107548; Traf5.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf_TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00061; MATH; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Receptor; Zinc-finger.
SQ   SEQUENCE 558 AA; 64145 MW; 48F64FB83BD587E5 CRC64;
```

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Query Match   41.7%; Score 1253.5; DB 11; Length 558;
Best Local Similarity 42.9%; Pred. No. 8.9e-71;
Matches 243; Conservative 116; Mismatches 176; Indels 31; Gaps 11;

Qy   22  HTDRSAGTP-VFVPEQGG------------YKEKFVKTVEDKYKCEKCHLVLCSPKQTECGH  70
             |::  :| :|                  ||:  :| :||| :|   | |  |||| |||
Db    3  HSEEQAAVPCAFIRQNSGGNSISLDFEPDTEYQFVEQLEERYKCAFCHSVLHNPHQTGCGH  62

Qy   71  RFCESCMAALLS-SSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNESRGCAEQLT  129
          |||  | ::|  |:| ||  ||:||||  |:|||||||||:| | |||:   |||| ::
Db   63  RFCQOCIRSLRELNSVPICPVDKEVIKPQEVFKDNCCKREVLNLHVYCKN-APGCNARII  121

Qy  130  LGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIAL  189
          ||  | :| :|  | ||||  |||||| |||||| |:||||||||| ||:|| |||:|:
Db  122  LGRFQDHLQH-CSFQAVPCPNESCREAMLRKDVKEHLSAYCRFREEKCLYCKRDIVVTNL  180

Qy  190  QKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIK  249
          | |: ||  ||:| || |:||| | |||||||||||:| |  |  ||||| | ||||||
Db  181  QDHEENSCPAYPVSCPNRC-VQTIPRARVNEHLTVCPEAEQDCPFKHYGCTVKGKRGNLL  239

Qy  250  AHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEML  309
          : | ::  ||::::|   :|  |:  | |:::|:| |||| |  ||  |||  ||::|::
Db  240  EHERAALQDHMLIVLEKNYQLEQRISDLYQSLEQKESKIQQLAETVKKFEKELKQFIQMF  299

Qy  310  RNNESKILHLQRVIDSQAEKLKELDKEIRPFRQ--NWE----EADSMKSSVESLQNRVTE  363
          ||   :|:| |:|  | :|::|  | |  |     | |      : :|:|::|::|| |
Db  300  GRNGTFLSNVQ-ALTSHTDKSAWLEAQVRQLLQIVNQQPSRLDLRSLDVADSVKQRITQ  358

Qy  364  LESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIIRLADMDLRFQVLETASYNGVLIWKIR  423
          ||| |   |:| ::| :|||||| ||||::|:||:|:|||||||||| :: :| ||||  |
Db  359  LEASD------QRLVLEGETSKHDAHINIHKAQLNKNEERFKQLEGACYSGKLIWKVT    411

Qy  424  DYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYD  483
          ||  ||:|||  ::||| |||||| |  |:|||| |||||| ||||||||:||::|||:|
Db  412  DYRVKKREAVEGHTVSVFSQPFYTSRCGYRLCARAYLNGDGSGKGTHLSLYFVVMRGEFD  471

Qy  484  ALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSSFKKPTGEMNIASGCPVFVAQTVL  543
          :|| ||||:|||||||||  :: ||  ||| || |||||||:| |||||||| ||: ||
Db  472  SLLQOWPFRQRVTLMLLDQSGKKNHIVETFKADPNSSSSFKRPDGEMNIASGCPRFVSHSTL  531

Qy  544  EN--GTYIKDDTIFIKVIVDTSDLPD                                    567
          |   |||||||:|:||:|||:|| |
Db  532  ENSKNTYIKDDTLFLKVAVDLTDLED                                    557
```

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RESULT 3
ID   O00463
AC   O00463;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF5 (TNF receptor associated factor 5).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
```

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RX   MEDLINE-9172745; PubMed-9511754;
RA   Mizushima S., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA   Otsuka M., Yamamoto T., Inoue J.;
RT   "Cloning and characterization of a cDNA encoding the human homolog of
RT   tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL   Gene 207:135-140(1998).
RN   [2]
RP   SEQUENCE OF 20-557 FROM N.A.
RX   MEDLINE-97321041; PubMed-9177772;
RA   Nakano H., Shindo M., Yamada K., Yoshida M.C., Santee S.M., Ware C.F.,
RA   Jenkins N.A., Gilbert D.J., Yagita H., Copeland N.G., Okumura K.;
RT   "Human TNF receptor-associated factor 5 (TRAF5): cDNA cloning,
RT   expression and assignment of the TRAF5 gene to chromosome 1q32.";
RL   Genomics 42:26-32(1997).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AB000509; BAA25262.1; -.
DR   EMBL; U69108; AAC51329.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ   SEQUENCE   557 AA;  64405 MW;  86EB3724CE111176 CRC64;

Query Match             39.68%;  Score 1192.5;  DB 4;  Length 557;
Best Local Similarity   42.0%;  Pred. No. 5.9e-67;
Matches  232;  Conservative  121;  Mismatches  178;  Indels  21;  Gaps  9;

Qy     25 RSAGTPVFVPEQGGYKEKFVKTVEDKYKCEKCHLVLCSPKQTECGHRFCESSCMAALLS-S  83
          ::::||  |||  ||||:|:|: :|||||:||:|||||:| ||:| ||||| ||  ||:|
Db     17 QNSGNSISLDFEPSIEVQFVERLEERYKCAPCHSVLHNPHQTGCGHRFCQHCILSLRELN  76

Qy     84 SSPKCTACQESIVKDKVFKDNCCKRETLALQIYCRNESRGCAEQLTLGHLLVHLKNDCHF  143
Db     77 TVPICPVDKEVIKSQEVFKDNCCKREVLNLVYCSN-APGCNAKVILGRYQDHLQ-QCLF  134

Qy    144 EELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVS  203
Db    135 QPVQCSNEKCREPVLRKDLKEHLSASCQFRKEKCLYCKKDVVINLQNHEENLCPEYPVF  194

Qy    204 CPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLL  263
Db    195 CPNNCA-KIILKTEVDEHLAVCPEAEQDCPFKHYGCAVTDKRRNLQQHEHSALREHMRLV  253

Qy    264 KEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILHILQRVI  323
Db    254 LEKNVQLEEQISDLHKSLEQKESKIQQLAETIKKLEKEFKQFAQLFGKNGSFLPNIQ-VF  312

Qy    324 DSQAEKLKELDKEIRPF------RQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARN  377
Db    313 ASHTDKSAWLEAQVHQLLQMVNOQQNKFDLRPLMEAVDTVKQKITLLENND------QR  365

Qy    378 TGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKT  437
Db    366 LAVLEEETNKHDHIHINIHKAQLSKNEERFKLLEGTCYNGKLIWKVTDYKMKREAVDGHT  425

Qy    438 LSLYSQPFYTGFGYKMCARVYLNGDGMGKGTHLSLSLFFVIMRGEYDALLPWPFKQKVTLM  497
Db    426 VSIFSOSFYTSRCGYRLCARAYLNGDGSGRGSHLSLYFVVMRGEFDSLLQWPFRQRVTLM  485

Qy    498 LMDGGSSRRHLGDAFKPDPNSSSSFKKPTGEMNIASGCGVFVAQTVLEN--GTYIKDDTIF  555
Db    486 LLDQ-SGKKNIMEIFKPDPNSSSKRPDGEMNIASGGCPRFVAHSVLENAKNAYIKDDTLF  544

Qy    556 IKVIVDTSDLPD  567
Db    545 LKVAVDLTDLED  556
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RESULT 4
ID   O54896            PRELIMINARY;      PRT;   508 AA.
AC   O54896;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor associated factor 2A.
GN   TRAF2A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=KIDNEY;
RX   MEDLINE-98129826; PubMed-9461607;
RA   Brink R., Lodish H.F.;
RT   "Tumor necrosis factor receptor (TNFR)-associated factor 2A (TRAF2A),
RT   a TRAF2 splice variant with an extended RING finger domain that
RT   inhibits TNFR2-mediated NF-kappaB activation.";
RL   J. Biol. Chem. 273:4129-4134(1998).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AF027570; AAC53545.1; -.
DR   HSSP; P12351; 1HWT.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM000061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Receptor; Zinc-finger.
SQ   SEQUENCE   508 AA;  56757 MW;  74B8B26BFCF9B1C4 CRC64;

Query Match             27.7%;  Score 832;  DB 11;  Length 508;
Best Local Similarity   33.7%;  Pred. No. 2e-44;
Matches  199;  Conservative  90;  Mismatches  190;  Indels  112;  Gaps  19;

Qy      3 SSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKT-VEDKYKCEKCHLVLC  61
          :|  :| :||  ::  |         ::::||  |||  ||||:||: :|||||:||:|||||:
Db      2 AAASVTSPGSLELLQP--------------GFSKTLLGTRLEAKYLCSACKNILR  42

Qy     62 SPKQTECGHRFCESCM-----AALLSSSSPK-CTAC------QESI--VKDKVFKDNC  105
          :||:| |||||:||:||     ||:|||| |  ||||      |||:  |||||||||:
Db     43 RPFQAQCGHRYCSFCLTSILRCASILSSSGPQNCACVYEGLYEEGISILESSSAFPDNA  102

Qy    106 CKREILALQIYCRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDH  165
          :||::|:| ||||  |:||:|||:||||:||||:|:|||| ||:||||||:||||||:
Db    103 ARREVESLPAVCPND--GCTWKGTLKEYESCHEGLCPFLLTEC--FACKGLVRLSEKEHH  158

Qy    166 VEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSEC  225
          ::|:|:||:::|||||||:|:|:::|:||: ||:|:::|| ||:|:| |||:|:|:
Db    159 TEQECPKRSLSCQHCRAPCSHVDLEVHEV-CPKFPLIC-DGCGKKKIPRETFQDHVRAC  216

Qy    226 VNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVS---------  275
          :|: | |:||:  |:::|:|:|:||||:::|:|||:||||:|:|:|||:|
Db    217 SKCRVLCRFHTVGCSEMVETENLQDHELQRLREHLAJLL--LSSFLERAQASPGTLNQVGPE  274

Qy    276 LLQNESVEKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILHLQRVIDSQAEKLKELDK  335
          |||:| :|:| |||:|||| || | |:|:|:|:|||::||||:|||: |||:|:|:|:|
Db    275 LLQRCQILEQK-IATFENIVCVLNREVER---------VAVTAEACSRQHRLDQ  318

Qy    336 EIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVH  395
          :|:|: :|:||||||||||:||||||||||:||||:|||:||||||:|:|||||:|:|:|
Db    319 D----------------------KIEALSNKVQQLE-----RSIGL  338

Qy    396 DIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGFGYKMC  455
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Db  339  DLAMADLEQKVSELEVSTYDGVFIWKISDFTRKRQEAVAGRIPAIFSPAFYTSRYGYKMC 398
         ||:||||||| ||||:||||||||||||||:|||||||||||:||||||||||||||
Qy  456  ARYYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPD 515
         |||||||||:|:||||||||||:||| ||||:|||:|||||||||: ||||:|||||:||
Db  399  LRVYLNGDGTGRGTHLSLFFVVNKGPNDALLQWPFNQKVTLMLLDH-NNREHVIDAFRPD 457
Qy  516  PNSSSFKKPTGEMNIASGCPVFVAQTVLE-NGTYIKDDTIFIKVIVDITSDL 565
         ::|||| || :|||||||||:| || : |  :||:|||:|||||:||| |||
Db  458  VTSSSFQRPVSDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 508
```

```
RESULT 5
ID   Q96NT2                 PRELIMINARY;      PRT;    447 AA.
AC   Q96NT2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CDNA FLJ30124 fis, clone BRACE1000093, highly similar to TNF receptor
DE   associated factor 2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CEREBELLUM;
RA   Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA   Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA   Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA   Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA   Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA   Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AK054686; BAB70792.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 1.
KW   Zinc-finger.
SQ   SEQUENCE  447 AA;  49377 MW;  73E158E346AB31D7 CRC64;

Query Match     23.8%;
Best Local Similarity   31.6%;    Score 717;  DB 4;  Length 447;
Matches  178;  Conservative  73;  Mismatches  147;  Indels  166;  Gaps  16;

Qy   36  QGGYXEKFVKT-VEDKYKCEKCHLVLCSPKQTECGHRPCESCMAALLSSSSSPKCTAC-QE  93
         |:|: ||:|    ||:|||||||||||:|||||||||||||||||||||||||| :|
Db   16  QPGFSKTLLGTKLEAKYLCSACRNVLRPFQAQCGHRYCSFCLASILSSGPQNCAACVHE  75

Qy   94  SIVKDKV------------FKDNCCKREILALQIYCRNESRGGAEQLTLGHLLVHLKNDCHFEE 145
         :|:|||             ||||||||| ||| |:|||| |:||||| |:|||||:| |:
Db   76  GIYEEGISILESSSAFFDNAARREVESLPAVC--PSDGCTWKGTLKEYEVKMPACGMVTE 133

Qy  146  LPCV-----RPDCKEKVLRKD-------------LRDHVEKACKYREATCSHCKS 182
         | |      ||||:||:|:|               |:| |:||:||| |||| |
Db  134  APAVGSRPRSPSSYDLVLHVPLLGAEACLMSVEEETELLLRSCHEGRCPLMLTECPACKG 193

Qy  183  QVPMIALQXHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQ 242
         | ||||: |:| ||||||||||||||||||||:|||:|||| ||| ||||| |||| ||
Db  194  LVRLGEKRHLEHCPERSLSCRI-CRA-PCCADVKAHHEVCPKFPLTCD---GCG- 245

Qy  243  GTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEI 302
         :|:|                                              :|:
Db  246  -------------------------------------------------KKKI 249
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Qy  303  ERQKEMLRNNESKILIHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRVT 362
         ::|:|   |: :|  :|  :|| |||:|:|| |:: :|||::|||  |  :  ||:|||
Db  250  -----------------------------PREKFQDQOK---------IEALSSKVQ 268

Qy  363  ELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGVLIWKI 422
         :|:: || :||:|| | ||:|| ||: ::|: :|| ||:| |:| :||:|: |||||||
Db  269  QLE------------RSIGL-------------KDLAMADLEQKVLEMEASTYDGVFIWKI 304

Qy  423  RDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARYLNGDGMGKGTHLSLFFVIMRGEY 482
         |||:|:|:|:|: |||  |||| | |||| ||| |||||||| ||||||||||:|||||
Db  305  SDFARKRQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPN 364

Qy  483  DALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTV 542
         ||||:| ||||||||||||||||||| ||||| ||||||||||||||||||||||||| |
Db  365  DALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSK 423

Qy  543  LE-NGTYIKDDTIFIKVIVDITSDL 565
         |: |||||||||||||||||||||
Db  424  MEAKNSYVRDDAIFIKAIVDLTGL 447
```

```
RESULT 6
ID   Q90WT6                 PRELIMINARY;      PRT;    501 AA.
AC   Q90WT6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 19, Last annotation update)
DE   Tumor necrosis factor receptor associate factor-2.
GN   TRAF2.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang T., Secombes C.J.;
RT   "Cloning and expression of crucian carp tumor necrosis factor receptor
RT   associate factor-2 (TRAF2).";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AJ297860; CAC82653.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
KW   Receptor; Zinc-finger.
SQ   SEQUENCE  501 AA;  56503 MW;  DE0ED0F8D9DCC287 CRC64;

Query Match     23.0%;
Best Local Similarity   30.7%;    Score 692;  DB 13;  Length 501;
Matches  159;  Conservative  84;  Mismatches  169;  Indels  106;  Gaps  14;

Qy   40  KEKFVKTVEDKYKCEKCHLVLCSPKQTECGHRPCESCMAALLSSSSSPKCTACQ-ESIVKD  98
         :|: ||:|||||||||||||||||:|||||||||||||||||||||||||||| :|:||
Db   32  REVLSVSMEPKYCQQCKEILRKPFQAQCGHRFCVFCFKQLTSSGPIPCEACRAEGIFEE  91

Qy   99  KV-----FKDNCCKREILALQIYCRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVR 150
         |:      ||||:||||||||||||||||||||||||||||||||||:|||:|||| |
Db   92  AMSMINITVAFPDNAARREIDSLPAKCPND--GCSWSGTLKDYEGQOHEGRCDFERVKC-- 147

Qy  151  PDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSV 210
         |||||||||:|:| |:||:|| |||||||||||| ||||||:||:|||||||||||||||
Db  148  EACQAVILSEKDRHNERECEARTLNCKYCKVTFNFKEIKAHDEI-CQKFPMQC-KDCGK 205

Qy  211  QTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLL------ 263
         |||| |||:|||||||||||||| |||||||||| :||||||||:|| |||||
Db  206  KKIPREKFQEHTKSCARKSKSACQFSEIGCRAVVDNGKQQEHEQTSVMEHLRIMLSVLSSV 265
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Qy    264  ------KEWSNSLEKKVSLLQ-----NESVEK-------NKSIQSLHNQICS  297
                 |:|                 |:           :|::|:|:|
Db    266  RLRAEGAEWQE--DSGLGLYRGPEDAPPAGPNAAAHNAGRGGGPGVQOKVTALENIVCV  323

Qy    298  FEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESL  357
                 |:|                                        ||:|
Db    324  LNREVERSALTL-----------EALSRQHRLDQE----------KIENL  352

Qy    358  QNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGV  417
           |||||  ||  ||                                   :: |
Db    353  SNKVRQLE------------------RTLTMRDLQLAESEQSLRELQFCTYDGV  388

Qy    418  LIWKIRDYKYRRKQEAVMGKTLSLIYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVI  477
           |||| || ||| ||:|  | :| |:|:||||||||||||||||||||:|||||||||
Db    389  FIWKIADFSRRRQDAVGGRAPAMFSPAFYSSKYGYKMCLRLYLNGDGTGRGTHLSLFFVV  448

Qy    478  MRGEYDALLPWPFKQKVTLMLMDQGSSRRHGDAFKPD  515
           ||||||||| ||||||| |||  ||:| |||:||
Db    449  MRGKYDALLKWPFSQKVTLMLLDQ-NNREHIDAFRPD  485
```

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RESULT 7
Q14848

ID   Q14848;          PRELIMINARY;      PRT;      470 AA.
AC   Q14848;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cystein rich domain associated to RING and TRAF protein.
GN   MLN 62, CAR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BREAST DERIVED METASTATIC LYMPH NODE;
RX   MEDLINE=96039245; PubMed=7490069;
RA   Regnier C.H., Moog-Lutz C., Mattei M.G., Chenard M.P.,
RA   Lidereau R., Basset P., Rio M.C.;
RT   "Presence of a new conserved domain in CART1, a novel member of the
RT   tumor necrosis factor receptor-associated protein family, which is
RT   expressed in breast carcinoma.";
RL   J. Biol. Chem. 270:25715-25721(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BREAST DERIVED METASTATIC LYMPH NODE;
RX   MEDLINE=98029665; PubMed=7592751;
RA   Regnier C.H., Tomasetto C., Chenard M.P., Wendling C.,
RA   Masson R., Regnier C.H., Chenard M.P., Wendling C.,
RA   Tomasetto C., Rio M.C.;
RT   "Identification of four novel human genes amplified and overexpressed
RT   in breast carcinoma and located to the q11-q21.3 region of chromosome
RT   17.";
RL   Genomics 28:367-376(1995).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; X80200; CAA56491.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 3.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ   SEQUENCE   470 AA;  53443 MW;  5D457E05A78770E2 CRC64;
```

```
Query Match             18.6%;  Score  560.5;  DB 4;  Length 470;
Best Local Similarity   24.9%;  Pred. No. 1.9e-27;
Matches  147;  Conservative   75;  Mismatches 173;  Indels 195;  Gaps 13;
```

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Qy    38  GYKEKFVKTVEDKYKYCEKCHLVLCSPKQ-TECGHRFCESCMAALLSSSSPKCTACQESIV  96
              ||:|:|| ::::: |:|    |  :    | ||| ||| || |:||  :  ||||
Db     3  GPDYKFLEKPKRRLLCPLCGKPMREPVQVSTCGHRFCDTCLQEFLSEGVFPKCPEDQLPLD  62

Qy    97  KDKVFKDNCCKREILALQIYCRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVRPD-CKE  155
                 |  :   |||:||
Db    63  YAKIYPDPELEVQLGLPIRCIHSEEGCRWSGPLRHLQGHL-NTCSFNVIPC--PNRCPM  119

Qy   156  KVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHE------------------------  193
              |:  :                |:
Db   120  KLSRRDLPAHLQHDCPKRRLKCEFCCGCDFSGEAYESHEGMCPQESVYCENKCGARMMRGL  179

Qy   194  -----------------DT-------DCPCVVVSCPHKCSVQTLLRSELSAHL  222
                             ||         :||| |||:: :| |   |: ||
Db   180  LAQHAISECPKRTQPCTYCYTKREFVFDTIQSHQYQCPRLPVACPNQCGVGTVAREDLPGHL  239

Qy   223  SE-CVNAPSTCSFKRYGCVFQGTNQOIKAHEASSAVQHVNILKEWSNSLEKKVSLLQENS  281
              |                        |      ::          ::  ::
Db   240  KDSCNTALVLCPFKDSGCKHRCPKLAMARHVEESVKPHLAMM----------------  281

Qy   282  VEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFR  341
               :|                                   |   ||||:|
Db   282  -----------------------------------------LVSRQQELQELRREL---  299

Qy   342  QNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLAD  401
                      |                           |:| :||:|
Db   299  ----------CA-----------------------------  299

Qy   402  MDLRFQVLETASYNGVLIWKIRDYKYRRKQEAVMGKTLSLIYSQPFYTGYFGYKMCARVYLN  461
                     :||||  | :|:|||:  ||  |:|   || :|   |:||||| | ||||:|
Db   305  -------GSDGVLIWKIGSYGRRLQEAKAPKNLECFSPAFYTHKYGYKLQVSAFLN  353

Qy   462  GDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG----SSRRHLGDAFKPDPN  517
           |:| :|:|||||||:|| || |||| ||| | ||| :|:|       |:|| |||||||
Db   354  GNGSGEGTHLSLYIRVLPGAEFDNLEWPFARRVTFSLLDQSDPGLAKPQHVTETFHPDPN  413

Qy   518  SSSFKKP---------TGEMNIASGCPVFVAQTVLENGTYIKDDIFIKIVID  561
               :|:||                |:| :  :|   ||| :|  ||  ||
Db   414  WKNFQKPGTWRGSLDESSLGFGYPKFISHQDIRKRNVRDDAVFIRAAVE  463
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RESULT 8
Q9BU24

ID   Q9BU24;          PRELIMINARY;      PRT;      470 AA.
AC   Q9BU24;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TNF receptor-associated factor 4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EYE;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; BC001769; AAH01769.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
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DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 3.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Receptor; Zinc-finger.
SQ   SEQUENCE   470 AA;  53542 MW;  A3F57E0E1081AB88 CRC64;

Query Match             18.6%;  Score 560.5;  DB 4;  Length 470;
Best Local Similarity   24.9%;  Pred. No. 1.9e-27;
Matches  147;  Conservative  75;  Mismatches  173;  Indels  195;  Gaps  13;

Qy         38 GYKEKFVKTVEDKYKCEKCHLVLCSPKQ-TECGHRFCESCMAALLSSSSPKCTACQESIV  96
              :! :||| ||| : | ::| || ::|  ||:| || |: :|:  : :::  | | ::|
Db          3 GFDYKFLEKPKRRLLCPLCGKPMREPVQVSTCGHRFCDTCLQEFLSEGVFKCPEDQLPLD  62

Qy         97 KDKVFKDNCCKREILALQIYCRNESRGCAEQLILGHLLVHLKNDCHFEELPCVRPD-CKE  155
              : :: | |: :|  ||| : |||| ||| |::|: ||||||||||||||||||||| ||
Db         63 YAKIYPDPELEVVLGLPIRCIHSEEGCRWSGPLRHLQGHL-NTCSFNVIPC--PNRCPM  119

Qy        156 KVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHE---------------------  193
              ||:|:||||||| ::| |||||||||||||||||||||
Db        120 KLSRRDLPAHLQHDCPKRRRLKCEFCGGCDFSGEAYESHEGMCPQESVYCENKCGARMRRL  179

Qy        194 ------------------DCPCVVVSCPHKCSVQTLLRSELSAHL  222
                                ||:|:  | |||: |:|| :|
Db        180 LAQHATSECPKRTQPCYCTYCTKEEVFDTIQSHQYQCPRLPVACPNQCCGVGTVAREDLPGHL  239

Qy        223 SE-CVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQONES  281
              :: |:  ||||||:| |||:||||||:|| ||::: | ||:|||:|| |:||:|
Db        240 KDSCNTALVLCPFKDSCCKHRCPKLAMARHVEESVRPHIAMM--------------------  281

Qy        282 VEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFR  341
              ||::| :  || :| | | |||:|: |||:|::|::| |:  | :: :| : | :|
Db        282 --------------------------CA-----------------------------------  284

Qy        342 QNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLAD  401
              || ::
Db                                                   LVSRQRELQELRREL-----  299

Qy        402 MDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKILSLYSQPFYTGYFGYKMCARVYLN  461
              |||||::|:|  : ||| | | |
Db        305 ------GSDGVLIWKIGSYGRRLQERAKAKPNLECFSPAFYTHKYGYKLQVSAFLN  353

Qy        462 GDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG----SSRRHLGDAFKPDDN  517
              ||| ||||||||||||||||||||||||||||||||||||     ::||||||| || :
Db        354 GNGSGEGTHLSLYIRVLPGAFDNLLEWPFARRVTFSLLDQSDPGLAKPQHVTETHPDDN  413

Qy        518 SSSFKP-----------TGEMNIASGCPVPVAQTVLENGTYIKDDTIFIKVIVD  561
               :::|:              ::|:|| |:  :| : : ||:||||:|:||:||
Db        414 WKNFQKFPGTWRGSLDESSLGFGYPKFISHQDIRKRNYVRDDAVFIRAAVE  463
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RL   Nature 383:443-446(1996).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; U78798; AAB38751.1; -.
HSSP; P15919; 1RMD.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR000504; RNA_rec_mot.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ   SEQUENCE   522 AA;  59573 MW;  5AB9C255CCFEE749 CRC64;

Query Match             18.4%;  Score 553;  DB 4;  Length 522;
Best Local Similarity   26.7%;  Pred. No. 6.4e-27;
Matches  144;  Conservative  101;  Mismatches  199;  Indels  96;  Gaps  16;

Qy         32 FVPEQGGYKEKFVKTVEDKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTAC  91
              || : |||| | ::| || ::| ||||||||:|| |||||||:|::::::::::::|:||
Db         49 FMEEIQGYDVEFDPPLESKYECPICLMALREAVQTPCGHRFCKACIIKSIRDAGHKCPVD  108

Qy         92 QESIVKDKVFKDNCCKREILALQIYCRNESRGCAEQLILGHLLVHLKNDCHFEELPCVRP  151
              :|::  : | :||:||:|||| : ||| || |::|:::||||||||:|:|| ||:||::
Db        109 NEILLENQLFPDNFAKREILSLMVKCPNE---GCLHKMELRILEDH-QAHCEFALMDC--P  163

Qy        152 DCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQ  211
              :| :| |:||||||||||||||||||||||||||||||:: ||::|| :|||||:||:||
Db        164 QCQRPFQKFHINIHILKDCPRRQVSCDNCAASMAFEDKEIH-DQNCPLANVICEY-CNT-  220

Qy        212 TLLRSELSAHLS-ECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSL  270
              |||||||:||:  ||||||||||||||| :|| ||||:|| |:::| | ||:|||:|:||
Db        221 ILIREQMPNHVDLDCPTAPIPCTFSTFGGCHEKMQRNHLARHILQENTQSHMRMLAQAVHSL  280

Qy        271 EKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKL  330
              |:||:||:|||  ||:| :  || :| | | |||:|: ||:|::|::| |:  | :: :|
Db        281 -----SVIPDSGYIS---EVRNFQETIHQLEGRLVRQDHQIRELTAKMEIQSMTV  327

Qy        331 KELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQ  390
              | : |::|:||::|| ::  | |||:|:||||:|||| |:::| |:|||||||||||:||
Db        328 ----SELKRTIR-----------TLEDKVAEIEA-----------------------------  346

Qy        391 MLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDY---KRRKQEAVMGKTLSLYSQPFY  446
              |||| |:||: |:||||::|:|  : ||| | | |    |||:|| |:  :| :
Db        347 -----------QQCNGIYIWKIGNFGMHLKCQEEE----KPVVIHSPGFY  381

Qy        447 TGYFGYKMCARVYLN-GDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSS-  504
              ||| || : ||:||| ||| ||||||||||||||||||||||||||||:||:|||||  :
Db        382 TGKPGYKLCMRLHLQLPTAQRCANYISLFVHTMQGEYDSHLPWPFQGTIRLTILDQSEAP  441

Qy        505 -RRHLGDAFKPDDPNSSSFKKPTGEMNIAS-GCPVPVAQTVLENGTYIKDDTIFIKVIVDT  562
               ||||||| || ::| ::|| |||:|: |: ||:|||:||:||||:|||||:|:||:||:
Db        442 VRQNHEEIMDAKPELLAFQRPTIPRNPKGFGYVTFMHLEALRQRTFIKDDTLLVRCEVST  501
```

```
RESULT 9
ID   Q9Y4K3      PRELIMINARY;    PRT;    522 AA.
AC   Q9Y4K3;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF6.
DE   Putative interleukin 1 signal transducer.
GN   TRAF6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96434892; PubMed=8837778;
RA   Cao Z., Xiong J., Takeuchi M., Kurama T., Goeddel D.V.;
RT   "TRAF6 is a signal transducer for interleukin-1.";
```

```
RESULT 10
ID   P70196      PRELIMINARY;    PRT;    530 AA.
AC   P70196;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF6.
GN   TRAF6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
```

Left column

```
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Inoue J.;
RT   "TRAF6, a novel CD40 associated factor.";
RL   J. Biol. Chem. 0:0-0(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97067112; PubMed=8910514;
RA   Ishida T., Mizushima S., Azuma S., Kobayashi N., Tojo T., Suzuki K.,
RA   Aizawa S., Watanabe T., Mosialos G., Kieff E., Yamamoto T., Inoue J.;
RT   "Identification of TRAF6, a novel tumor necrosis factor receptor
RT   associated factor protein that mediates signaling from an amino
RT   terminal domain of the CD40 cytoplasmic region.";
RL   J. Biol. Chem. 271:28745-28748(1996).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; D84655; BAA12705.1; -.
DR   HSSP; P15919; 1RMD.
DR   MGD; MGI:108072; Traf6.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR000504; RNA_rec_mot.
DR   InterPro; IPR003007; MATH.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ   SEQUENCE   530 AA;   60082 MW;   092D820B4CEDB85B CRC64;

Query Match             17.8%;  Score 536;  DB 11;  Length 530;
Best Local Similarity   25.7%;  Pred. No. 7.5e-26;
Matches  141;  Conservative   97;  Mismatches 206;  Indels 104;  Gaps  17;

Qy   32 FVPEQGGYKEKFVKTVEDKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTAC 91
Db   49 FMEEIQGYDVEFDPPLESKYECPICLMALREAVQTPGGHRFCKACIIKSIRDAGHKCPVD 108

Qy   92 QESIVRDKVFKDNCCKREIIALQIYCRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVRP 151
Db  109 NEILLENQLFPDNFAKREILSLTVKGPN--KGCLQKMELRHLEDH-QVHCFFALVNC--P 163

Qy  152 DCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKH-EDTDCPCVVVSCPHKCSV 210
Db  164 QCQRPFQKCQVNTHIIEDCPRRQVSCVNC--AVSMAYEKEIHDQSCPLANIICEY-CGT 220

Qy  211 QTFLLRSELSAHLS-ECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNS 269
Db  221 -ILIREQMPNIYDLDCPTAPICPTFSVFEGHQKMQRNHLARHLQENTQLHMRLL------ 273

Qy  270 LEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILHLQRVIDSQAEK 329
Db  274 ------------------AQAVHVNLAL----------------------- 292

Qy  330 LKELDKEIRPRQNMEEADSMKSSVESLQNRV----------------------- 378
Db  293 --SRGCRPEDPNYEE--------TIKQLESRLVRQDHQIRELTARKMETQSMYVGELKRTI 342

Qy  379 GLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTL 438
Db  343 RTLEDKVAE------------MEAQQCNGIYIWKIGKFGMHLKSQEEERPV 381

Qy  439 SLYSQPFYTGYGFYKMCARVYLN-GDGMGKGTHLSLFFVIMRGEYDALLPWPFRQKVTLM 497
Db  382 VIHSPGFYIGRPGYKLCMRLHLQLPTAQRCANYISLFVHTMQGEVDSHLFWPFQGTIRLT 441

Qy  498 LMDQGSS--RRHLGDAFKPDPNSSSSFKKPTGEMNIAS-GCPVFVAQTVLENGTYIKDDTI 554
Db  442 ILDQSEALIRQNHEEVMDAKPELLAFQRPTIPRNPKGFGYGVTFMHLEALRQGTFIKDDTI 501
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Right column

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Qy  555 FIKVIVIDT 562
Db  502 LVRCEVSVT 509

RESULT 11

ID   Q61382    PRELIMINARY;   PRT;   470 AA.
AC   Q61382;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cysteine rich motif associated to Ring and Traf domains protein
DE   (MCARI1).
GN   TRAF4 OR CART1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98175888; PubMed=9507120;
RA   Masson R., Regnier C.H., Chenard M.P., Wendling C., Mattei M.G.,
RA   Tomasetto C., Rio M.C.;
RT   "Tumor necrosis factor receptor associated factor4 (TRAF4) expression
RT   pattern during mouse development.";
RL   Mech. Dev. 71:187-191(1998).
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; X92346; CAA63103.1; -.
DR   MGD; MGI:1202880; Traf4.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; MATH.
DR   InterPro; IPR001841; znf_ring.
DR   InterPro; IPR001293; znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF02176; zf-TRAF; 3.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
KW   Zinc-finger.
SQ   SEQUENCE   470 AA;   53418 MW;   842F2168A926BAFB CRC64;

Query Match             17.4%;  Score 524.5;  DB 11;  Length 470;
Best Local Similarity   24.1%;  Pred. No. 3.4e-25;
Matches  142;  Conservative   75;  Mismatches 178;  Indels 195;  Gaps  13;

Qy   38 GYKEKFVKTVEDKYKCEKCHLVL-CSPKQTECGHRFCESCMAALLSSSSPKCTACQESIV 96
Db    3 GLDYKFPEKRKRLLCPLCSKPMRDSVEVSTCGHRYCDNCLQEFLSEGVFRKCPEDQLPLD 62

Qy   97 KDKVFKDNCCKREIIALQIYCRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVRPD-CKE 155
Db   63 YAKIYPDPELEVQVLGIARCIHSEEGCRWSGPLRHLQGHL-NTCSFNVVPC--PNRCPA 119

Qy  156 KVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHE------------------ 193
Db  120 KLSRDLPAHLQHDCPKRRLKCEFCGCDFSGEAYESHEGVCPQESVFCENKCGGARMMRRL 179

Qy  194 ----------------DT-----DCPCVVVSCPHKCSVQTLLRSELSAHL 222
Db  180 LAQHATSECPKRTQPCAYCTKEFVVDTIQSHQYQCPRLPVPCPNQCGVGTVAREDLPTHL 239

Qy  223 SE-CVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNES 281
Db  240 KDSCRTAFVLCPFKESGCKHRCPKLAMGRHVEESVKPHLAMM-------------- 281

Qy  282 VEKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFR 341
Db  282 --------------CA---- 299

Qy  342 QNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLAD 401
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Db   300 ------------------------------------------------EELSI------ 304

RESULT 12
Q9BIW7
ID   Q9BIW7        PRELIMINARY;      PRT;    462 AA.
AC   Q9BIW7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   TRF-1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21407711; PubMed=11516642;
RA   Pujol N., Link E.M., Liu L.X., Kurz C.L., Alloing G., Tan M.,
RA   Ray K.P., Solari R., Johnson C.D., Ewbank J.J.;
RT   "A reverse genetic analysis of components of the Toll signaling
RT   pathway in Caenorhabditis elegans.";
RL   Curr. Biol. 11:809-821(2001).
DR   EMBL; AF348168; AAK37546.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
SQ   SEQUENCE  462 AA;  52354 MW;  E07F04BF1756B343 CRC64;

Query Match             17.4%;  Score 522.5;  DB 5;  Length 462;
Best Local Similarity   26.1%;
Matches  136;  Conservative  69;  Mismatches  188;  Indels  129;  Gaps  12;

Qy    402 MDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLSLYSQPFYTGYGYKMCARVYLN 461
          :|||||| | |   |||  :|| |    ||:| ||:|||||:||||  :||| ||||||:||
Db    305 ----GSDGVLIWKIGSYGRRLQEAKAKPNLECFSPAFYTHKYGYKLQVSASLN 353

Qy    462 GDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG-----SSRRHLGDAFKPDPN 517
          ||  |||||| :|||  ||||| ||||||:|||||||| ||     |::||||||||||||
Db    354 GNGSGESTHLSIYIRVLPGAPDNLLEWPLARRVTFSLLDQSDPGLAKPQHYTETHPPDN 413

Qy    518 SSSFKKP---------TGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVD 561
          |::|: :         |||||:|||||||||:|||:|||||||:|||:|||||
Db    414 WKNFQKPGTWRGSLDESSLGFGYPKFISHQDIRKRNYVRDDAVFIRASVE 463
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RESULT 13
O62248
ID   O62248        PRELIMINARY;      PRT;    509 AA.
AC   O62248;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   F45G2.6 protein.
GN   F45G2.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lindsay S.J.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C. elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z93382; CAB07615.1; -.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001841; Znf_ring.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF02176; zf-TRAF; 2.
DR   SMART; SM00061; MATH; 1.
DR   SMART; SM00184; RING; 1.
SQ   SEQUENCE  509 AA;  57514 MW;  CFA0E068F5AD00C8 CRC64;

Query Match             17.4%;  Score 522.5;  DB 5;  Length 509;
Best Local Similarity   26.1%;
Matches  136;  Conservative  69;  Mismatches  188;  Indels  129;  Gaps  12;

Qy    412 ASYNGVLIWKIRDYKRRKQEAVMGKTLSLSLYSQPFYTGYGYKMCARVYLNGDGMGKGTHL 471
          :    |||||| | |   |||  :|| |    ||:| ||:|||||:||||  :||| ||||||:
Db    261 --FGPQLIWKIDKLQQRTNEAKSGADTTIPFSVPFMSHRFGYKMMACACLFGDGSSAGKSI 318

Qy    472 SLFFVIMRGEYDALLPWPFKQKVTLMLMDQGS------SRRHLGDAFKPDPNSSSFKKPT 525
          |||  ||||| ||||||:|||||||||| ||       |::||||||||||||
Db    319 SIYVLLKGEFDPTLEWPFHRAIKISLLDQNPRPEDRVNITYVIDPRKLKANEKFLARPR 378

Qy    526 GEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVDTSD-LP 566
          |||||:|||||||||:|||:|||||||:|||:|||||
Db    379 GERNAAPGSQSFCSLAILQN--YVKDDKIYVQIDVDRCETLP 418
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Qy     53 CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQQESIVKDKVFKDNCCKREILA 112
          :| |: : |  ||  || ||| ||:||||||| | || ||| :|| |::| |||||| ||
Db     18 CPICEQALRDPIKLNCDHHYCRQCFEN--ENRTPGCAACQTIIQPELCQOHDRAKQOILA 75

Qy    113 LQIYCRNESRGCAEQLIGHLLVHLKNDCHFE--ELPCVRPDCKEKVLRKDLRDHVEKACK 171
          | | ||| :| ||:|| |||||||:|||| |  ||||| ||| ::|||||||| || |:
Db     76 LPVVCTFESSGCPWDQGLGTLHDHL-SECTFKSSLKCEK--CGRQFAKNDLEKHRAK-CE 131

Qy    172 YREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPST 231
          |  | | |  :| | || :||  | | |  | ||:||| ::| | ||:| |  |  |  |
Db    132 LNRAVCSPCNKTIRDSDRERHPKT-CPQVIISCPFQCGLTDRPRLEIEAHCPSCPNVDNV 190

Qy    232 CSFKRYGCVFQGTNQOIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSL 291
          | | ||| | |::||:||:||| :|:|||::||||||||||||||||||||||||||:|||
Db    191 CPFVPYGCTFAGGKESIQQHLSDEPVRHLMYLCDEITDLKGTYELM-------------- 236

Qy    292 HNQICSFEIEIEROKEMLRNNESKIILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMK 351
          |::|||||||| ||:|:|| || :|:|| |||||||:||||||||||:|:||||||||||||
Db    237 -----ERDMGSFNDRQTRIL-------SAAETCTEM----------------------- 260

Qy    352 SSVESLQNRVTELESVDKSAGQVARNTGLLESOLSRHDQMLSVHDIRLADMDLRFQVLET 411
          :    :::||  :::|||  ||||
Db    261 ----------------------------------------------------------- 260
```

```
Qy     53 CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQQESIVKDKVFKDNCCKREILA 112
          :| |: : |  ||  || ||| ||:||||||| | || ||| :|| |::| |||||| ||
Db     65 CPICEQALRDPIKLNCDHHYCRQCFEN--ENRTPGCAACQTIIQPELCQOHDRAKQOILA 122

Qy    113 LQIYCRNESRGCAEQLIGHLLVHLKNDCHFE--ELPCVRPDCKEKVLRKDLRDHVEKACK 171
          | | ||| :| ||:|| |||||||:|||| |  ||||| ||| ::|||||||| || |:
Db    123 LPVVCTFESSGCPWDQGLGTLHDHL-SECTFKSSLKCEK--CGRQFAKNDLEKHRAK-CE 178

Qy    172 YREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPST 231
          |  | | |  :| | || :||  | | |  | ||:||| ::| | ||:| |  |  |  |
Db    179 LNRAVCSPCNKTIRDSDRERHPKT-CPQVIISCPFQCGLTDRPRLEIEAHCPSCPNVDNV 237

Qy    232 CSFKRYGCVFQGTNQOIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSL 291
          | | ||| | |::||:||:||| :|:|||::||||||||||||||||||||||||||:|||
Db    238 CPFVPYGCTFAGGKESIQQHLSDEPVRHLMYLCDEITDLKGTYELM-------------- 283

Qy    292 HNQICSFEIEIEROKEMLRNNESKIILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMK 351
          |::|||||||| ||:|:|| || :|:|| |||||||:||||||||||:|:|||||||||||
Db    284 -----ERDMGSFNDRQTRIL-------SAAETCTEM----------------------- 307
```

```
Qy  352 SSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLET ----- 411
        |||||||:|| |||||||||||||||||||||||:|||||||||||||||||||||||||
Db  308 ------                                                            307

Qy  412 ASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHL 471
        :||:|| ||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  308 ------                                                        307

Qy  472 SLFFVIMRGEYDALLPWPFKQKVTLMLMDQGS------ --SRRHLGDAFKPDPNSSSFKKPT 525
        :|:.|::.|| ||||| ||| |.|| .|  .|        ||||||||||||||||||:||:
Db  366 SLYVLLLKGEFDPFLEWPEPHRAIKISLLDQNRPEDRVNITVIVIDPRKLKANEKFLARPR 425

Qy  526 GEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVDFSD-LP 566
        ||||||:|| |||:|||||||||||||.|||:|| ||:|| ||
Db  426 GERNAAFGSQSFCSIAILQN--YVKDDKIYVQIDVDRCETLP 465
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RESULT 14
Q9XYR0

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ID   Q9XYR0          PRELIMINARY;      PRT;    486 AA.
AC   Q9XYR0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TRAF1 protein (LD20987p).
GN   TRAF1 OR CG3048.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99147085; PubMed=10021364;
RA   Liu H., Su Y.C., Becker E., Treisman J., Skolnik E.Y.;
RT   "A Drosophila TNF-receptor-associated factor (TRAF) binds the ste20
RT   kinase Misshapen and activates Jun kinase.";
RL   Curr. Biol. 9:101-104(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RA   Celniker S., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003576; AAF51024.1; -.
DR   EMBL; AF119794; AAD34346.1; -.
DR   EMBL; AY094792; AAM11145.1; -.
DR   FlyBase; FBgn0026319; Traf1.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001293; Znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF02176; zf-TRAF; 3.
DR   SMART; SM00061; MATH; 1.
KW   Receptor.
SQ   SEQUENCE FROM N.A.       486 AA;   53665 MW;   41474B5E014A99D5 CRC64;

Query Match             16.8%;  Score 506;  DB 5;  Length 486;
Best Local Similarity   24.3%;  Pred. No. 5.2e-24;  Indels 172;  Gaps 13;
Matches 140;  Conservative 77;  Mismatches 187;
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Qy    3 SSKKMDSPGCALQTNPPL-KLHYDRSAGTPVFVPEQQGYKEKPFVKTVEDKYKCE------ 54
          :  ||                || |  |  |      |  |    :|   :|
Db   67 SSHSSPTPGNNNNNMMPITELEQIIYPG-----PDPKHIMGSLVFCIHHKQGCKWSDELRK 121

Qy   55 -KCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDRVFKDNCCKREILAL 113
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Db  122 LKGHLNACKHDATQCPN------------------KCGAQIPRIMWTDHLQYTCTMRTRC- 164

Qy  114 QIYCRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYR 173
          : |  :   | : |:|  |:|||                |  |      |:||  ||:|
Db  165 -ERCQSEFSGAG-------LEEHNGSCGQEPVYC-EAKCGQRILRGRMTLHKSKDCAKR 214

Qy  174 EATCSHCKSQVPMIALQKHEDTDCPCVVVSCGPHKCSVQTLLRSELSAHL-SECVNAPSTC 232
          : ||  |  :  :  ||:|    | | | ||   |   | |  ||:|||  ||||  |  |
Db  215 LRRCAHCQREFSADTLPLHA-AQCPRAPLACPQRCDAGPIPRGELEAHLRDECQSLAVSC 273

Qy  233 SFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWNSLEKRVSLLQNESVEKNKSIQSLH 292
          ||: |||:.| : |:|:|||  :| ||  |
Db  274 SFKEAGCRFKGPRQMLEAHLESNAAHLSLMVALSSROGQOIQMI----------------- 318

Qy  293 NOICSFEIEIRQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKS 352
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Db  319 ------------------------------------------------------------KS 320

Qy  353 SVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETA 412
          :|  |                                                      |
Db  321 AVSKL-------------------------------------------------------SI 327

Qy  413 SYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLS 472
          .|.|:| ||| | |::|||:  | ||:| ||||| .||  |::||  |:|| || | :|:|
Db  328 NYTGLLWKITDWSAKMAEARGKDSLELVSPPFYTSQYGTYKLQASMFLNGNGPGENTHVS 387

Qy  473 LFFVIMRGEYDALLPWPFKQKVTLMLMDQG---SSRRHLGDAFKPDPNSSSFKPTGEMN- 529
          :: |::.||||||| ||| .:    ||:|      :  .| :|||||:  |  |
Db  388 VYIKVLPGEYDALLKWPFSHSITFLFEQGAQSGGGQVAESFVPDPTWENFQRSNEPDQ 447

Qy  530 IASGCPVFVAQTVLENGTYIKDDTIFIKVIVDFSDL 565
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Db  448 LGFGFPRFISHELLHSRPFIKGDTVFLRVDPSKI 483
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RESULT 15
Q9UAC5

ID   Q9UAC5        PRELIMINARY;      PRT;      412 AA.
AC   Q9UAC5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   TRAF1.
GN   TRAF1 OR CG3048.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Richter B.W.M., Duckett C.S.;
RT   "Identification of a Drosophila TRAF homolog.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Medzhitov R., Janeway C.;
RT   "Drosophila TRAF proteins are components of innate host defense
RT   pathways.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF079837; AAD47894.1; -.
DR   EMBL; AF111422; AAG21891.1; -.
DR   FlyBase; FBgn0026319; Traf1.
DR   InterPro; IPR002083; MATH.
DR   InterPro; IPR003007; TRAF.
DR   InterPro; IPR001293; znf_TRAF.
DR   Pfam; PF00917; MATH; 1.
DR   Pfam; PF02176; zf-TRAF; 3.
DR   SMART; SM00061; MATH; 1.
SQ   SEQUENCE   412 AA;  46159 MW;  81A05147AA7D64CE CRC64;

Query Match          16.7%;   Score 503;  DB 5;  Length 412;
Best Local Similarity 24.8%;  Pred. No. 6.5e-24;
Matches 129;  Conservative 73;  Mismatches 161;  Indels 158;  Gaps 10;

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Db     43  DELRKLKGHLNACKHDATQCPN-------------------KCGAQIPRIMMTDHLQYTCTMR 86

Qy    109  EILALQIYCRNESRGCAEQLILGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEK 168
               :|||   | | ||  |:|:|     |||:|    :|||:||:::|||:||:||:|
Db     87  RTRC--EFCQSEFSGAG-------LEEHNGSCGQEPVYC-EAKCGQRILRGRMTLHKSK 135

Qy    169  ACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHL-SECVN 227
               :||||  || ||   ||:|| |||||  | ||:|||||:| | | |:|:|  ||:||
Db    136  DCAKRLRRCAHCQREFSADTLPLHA-AQCPRAPLACPQRCDAGPIPRGELEAHLRDECQS 194

Qy    228  APSTCSFKRYGCVFQGTNQQIRAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKS 287
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Db    195  LAVSCSFKEAGCRFKGPRQMLEAHLESNAAAHLSLMVALSSRQGOQIQML----------- 244

Qy    288  IQSLHNQICSFEIEIEROKEMLRNNESKILIHLQRVIDSQAEKLKELDKEIRPFRONWEEA 347
               |:|:|  || |:|:: :: |||||||||||:|:|: |::|| |: |::::|: |:||:|
Db    245  -------------------------------------------------------------- 244

Qy    348  DSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQ 407
               |:|:|
Db    245  --KSAVSKL------------------------------------------------- 251

Qy    408  VLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLIYSQPFYTGYFGYKMCARVYLNGDGMGK 467
               : |.|.|||||:|:||:| |||:||||: ::|||:|  |:|||| | | :|::|| :|
Db    252  ---SINYIGTLLWKITDWSAKMAEAARGKDGLELVSPPFYTSQYGYKLQASMPLNGNGPGE 308

Qy    468  GTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG--SSRRHLGDAFKPDPNSSSFKKPT 525
               |::|:: || |||||||| | || ||||| |      :||||:|  ||| |:|| |||:
Db    309  NTHVSVYIKVLPGEYDALLKWPFSHSITFTLFEQGAQSGQGGVAESFVPDFTWENFQRPS 368

Qy    526  GEMN-IASGCPVFVAQTVLENGTYIKDDTIFIKVIVDTSDL 565
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Db    369  NEPDQLGFGFPRFISHELLHSRPFIKGDTIVFLRVKVDPSKI 409
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Search completed: December 19, 2002, 14:55:32
Job time : 42 secs